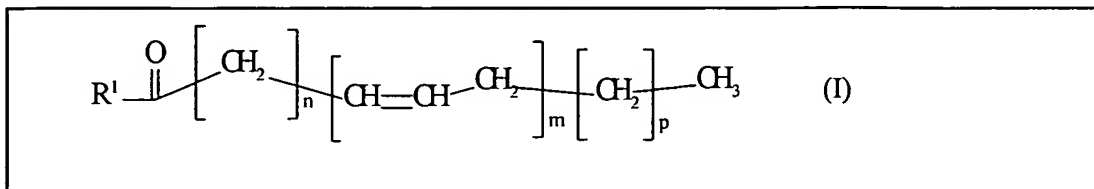
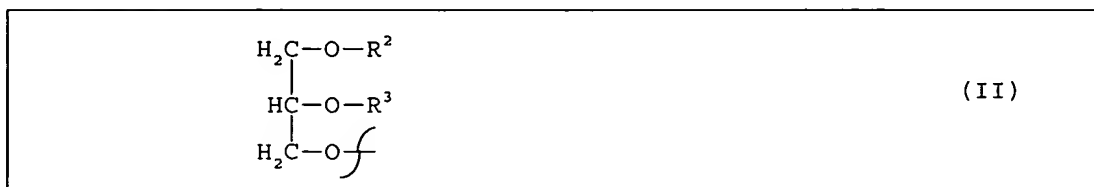


Clean Copy of Pending Claims 1-20

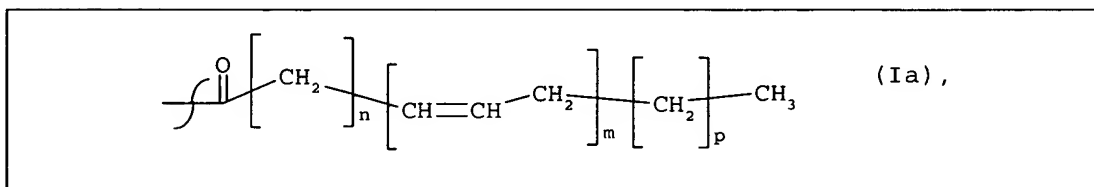
Claim 1. A process for the production of compounds in transgenic plants, wherein said compounds are comprised of general Formula I:



wherein $\text{R}^1 = -\text{OH}$, coenzyme A (thioester), phosphatidylcholine, phosphatidylethanolamine, phosphatidylglycerol, diphosphatidylglycerol, phosphatidylserine, phosphatidylinositol, sphingolipid, glycosphingolipid or a radical of general Formula II:



wherein $\text{R}^2 = \text{H}$, phosphatidylcholine-, phosphatidylethanolamine-, phosphatidylglycerol-, diphosphatidylglycerol-, phosphatidylserine-, phosphatidylinositol-, sphingolipid-, glycosphingolipid-, glycosphingolipid- or saturated or unsaturated $\text{C}_2\text{--C}_{24}$ -alkylcarbonyl-; and $\text{R}^3 = \text{H}$, saturated or unsaturated $\text{C}_2\text{--C}_{24}$ -alkylcarbonyl-; and wherein R^2 and R^3 independently of one another represent a radical of general Formula Ia:



wherein $n = 3, 4$ or 6 ; $m = 3, 4$ or 5 ; and $p = 0$ or 3 , and said compounds comprise at least 1% by weight of the total fatty acid content of said transgenic plants, which process comprises the following steps:

introducing into a plant:

at least one first nucleic acid sequence which encodes a polypeptide with an $\Delta 6$ -desaturase activity;

at least one second nucleic acid sequence which encodes a polypeptide with a $\Delta 6$ -elongase activity; and

optionally, a third nucleic acid sequence which encodes a polypeptide with a $\Delta 5$ -desaturase activity; and

growing and harvesting the transgenic plant.

Claim 2. The process of claim 1, wherein R^2 and R^3 independently of one another are C_{10} - C_{22} -alkylcarbonyl-.

Claim 3. The process of claim 1, wherein R^2 and R^3 independently of one another are C_{16} -, C_{18} -, C_{20} - or C_{22} -alkylcarbonyl-.

Claim 4. The process of claim 1, wherein R^2 and R^3 independently of one another are unsaturated C_{16} -, C_{18} -, C_{20} - or C_{22} -alkylcarbonyl- with one, two, three, four or five double bonds.

Claim 5. The process of claim 1, wherein the plant is an oil crop.

Claim 6. The process of claim 1, wherein the plant is selected from the group consisting of soya, peanut, oilseed rape, canola, linseed, evening primrose, verbascum, thistle, hazelnut, almond, macadamia, avocado, bay, wild roses, pumpkin/squash, pistachios, sesame, sunflower, safflower, borage, maize, poppy, mustard, hemp, castor-oil plant, olive, Calendula, Punica, oil palm, walnut and coconut.

Claim 7. The process of claim 1, wherein the compounds of general Formula I are obtained from the transgenic plants by pressing or extraction, and said compounds are in the form of oils, fats, lipids or free fatty acids.

Claim 8. The process of claim 7, wherein the oils, fats, lipids or free fatty acids are refined.

Claim 9. The process of claim 1, wherein saturated or unsaturated fatty acids present in the compounds are liberated.

Claim 10. The process of claim 9, wherein the saturated or unsaturated fatty acids are liberated by alkaline hydrolysis or enzymatic cleavage.

Claim 11. The process of claim 1, wherein the compounds comprise at least 5% by weight, of the total fatty acid content of the transgenic plants.

Claim 12. The process of claim 1, wherein the nucleic acid sequence that encodes the polypeptide with $\Delta 6$ -desaturase activity, $\Delta 6$ -elongase activity or $\Delta 5$ -desaturase activity is selected from the group consisting of:

a) a nucleic acid sequence that contains the sequence of SEQ ID NO: 1, SEQ ID NO: 3, SEQ ID NO: 5, SEQ ID NO: 7, SEQ ID NO: 9, SEQ ID NO: 11, SEQ ID NO: 13, SEQ ID NO: 15, SEQ ID NO: 17, SEQ ID NO: 19, SEQ ID NO: 21, SEQ ID NO: 23, SEQ ID NO: 25, SEQ ID NO: 27, SEQ ID NO: 29 or SEQ ID NO: 31,

b) nucleic acid sequences which, owing to the degeneracy of the genetic code, are obtained by back translation of an amino acid sequence contains the sequence of SEQ ID NO: 2, SEQ ID NO: 4, SEQ ID NO: 6, SEQ ID NO: 8, SEQ ID NO: 10, SEQ ID NO: 12, SEQ ID NO: 14, SEQ ID NO: 16, SEQ ID NO: 18, SEQ ID NO: 20, SEQ ID

NO: 22, SEQ ID NO: 24, SEQ ID NO: 26, SEQ ID NO: 28, SEQ ID NO: 30 or SEQ ID NO: 32,

c) derivatives of a nucleic acid sequence that contains the sequence of SEQ ID NO: 1, SEQ ID NO: 3, SEQ ID NO: 5, SEQ ID NO: 7, SEQ ID NO: 9, SEQ ID NO: 11, SEQ ID NO: 13, SEQ ID NO: 15, SEQ ID NO: 17, SEQ ID NO: 19, SEQ ID NO: 21, SEQ ID NO: 23, SEQ ID NO: 25, SEQ ID NO: 27, SEQ ID NO: 29 or SEQ ID NO: 31, which encode a derivative polypeptide that contains the amino acid sequence of SEQ ID NO: 2, SEQ ID NO: 4, SEQ ID NO: 6, SEQ ID NO: 8, SEQ ID NO: 10, SEQ ID NO: 12, SEQ ID NO: 14, SEQ ID NO: 16, SEQ ID NO: 18, SEQ ID NO: 20, SEQ ID NO: 22, SEQ ID NO: 24, SEQ ID NO: 26, SEQ ID NO: 28, SEQ ID NO: 30 or SEQ ID NO: 32, and which has at least 50% homology at the amino acid level, wherein enzymatic activity of the derivative polypeptide is not substantially reduced as compared to said polypeptide.

Claim 13. The process of claim 1, wherein one or more of the first, second, and optionally third nucleic acid sequences are linked with one or more regulatory signals in a nucleic acid construct.

Claim 14. The process of claim 13, wherein the nucleic acid construct comprises additional biosynthetic genes of fatty acid or lipid metabolism selected from the group consisting of acyl-CoA dehydrogenase(s), acyl-ACP [= acyl carrier protein] desaturase(s), acyl-ACP thioesterase(s), fatty acid acyl transferase(s), fatty acid synthase(s), fatty acid hydroxylase(s), acetyl-coenzyme A carboxylase(s), acyl-coenzyme A oxidase(s), fatty acid desaturase(s), fatty acid acetylenases, lipoxygenases, triacylglycerol lipases, allene oxide synthases, hydroperoxide lyases, fatty acid elongase(s) and combinations thereof.

Claim 15. The process of claim 1, wherein the first, second and optionally third nucleic acid sequences are stably integrated in the plant.

Claim 16. The process of claim 1, wherein the plant is selected from the group consisting of plant cells, plant tissues, plant organs, plant leaves, plant roots, plant stems, intact plants, plant tubers, plant seeds, and cellular parts of any of the preceding.

Claim 17. The process of claim 7, wherein the pressing or the extraction is performed without supplying heat.

Claim 18. The process of claim 12, wherein two or more of the first, second and third nucleic acid sequences are selected from said group.

Claim 19. The process of claim 12, wherein the first, second and third nucleic acid sequences are selected from said group.

Claim 20. The process of claim 13, wherein the first, second and third nucleic acid sequences are linked to with one or more regulatory signals in said nucleic acid construct.